Fig. 1

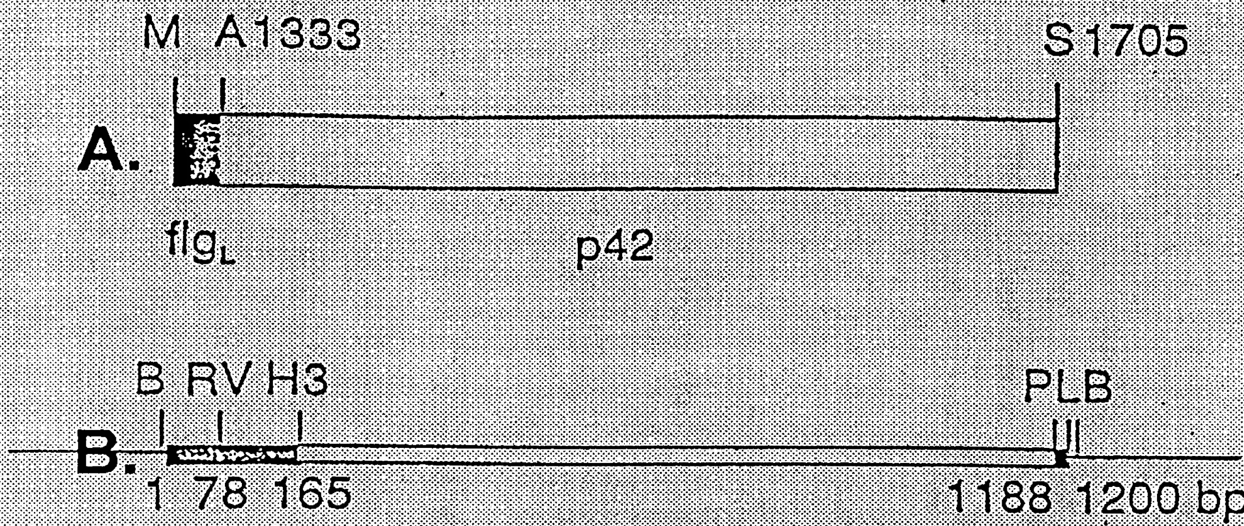


FIGURE 13

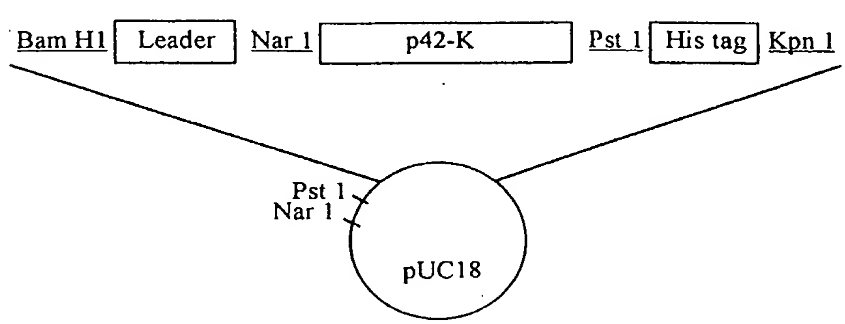


Fig. 2

Fig. 2A

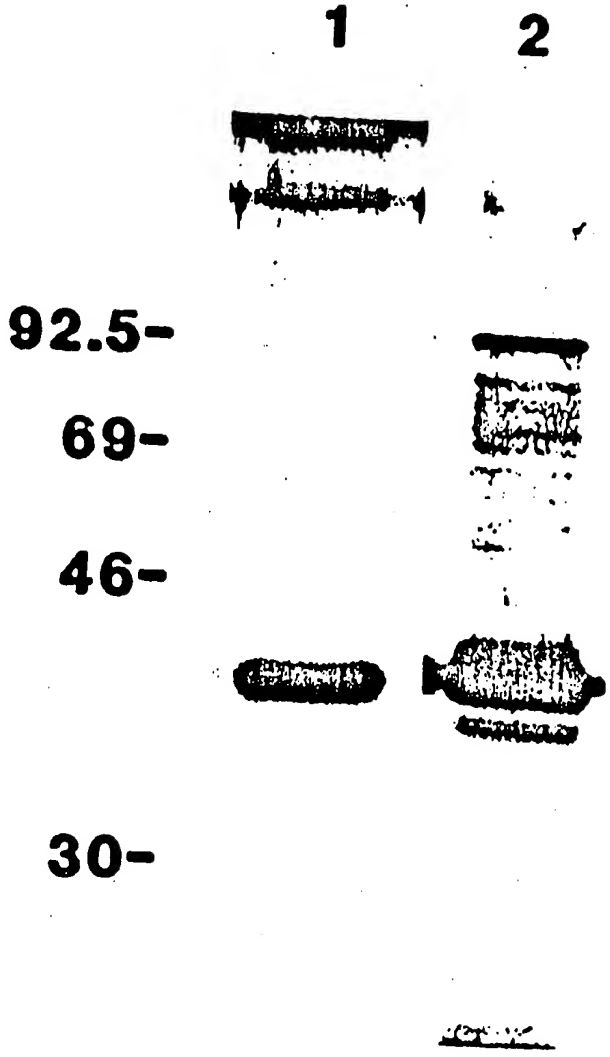


Fig. 2B

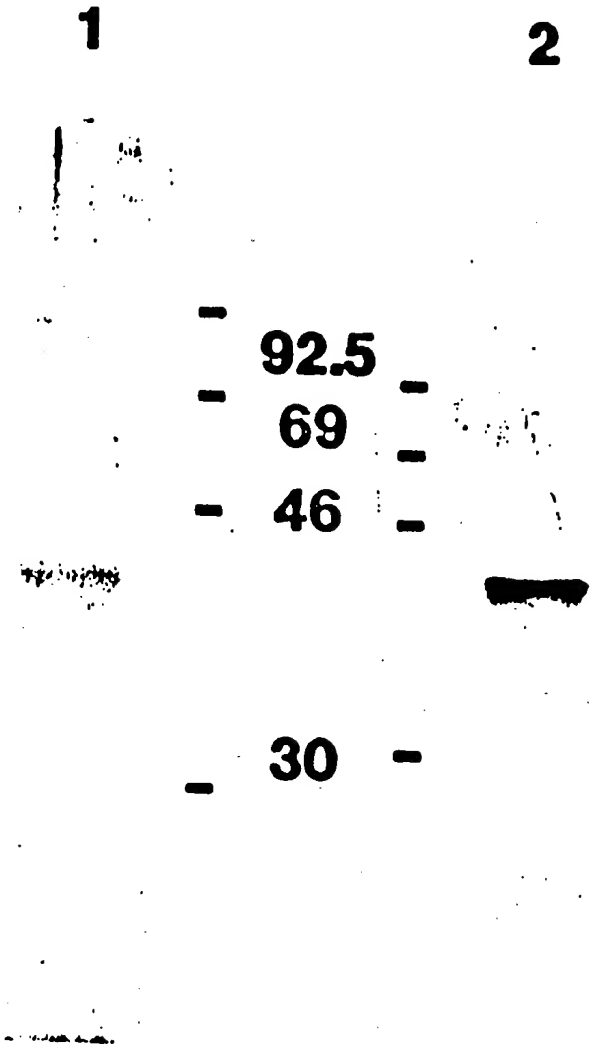


Fig. 3

Fig. 3A

Fig. 3B

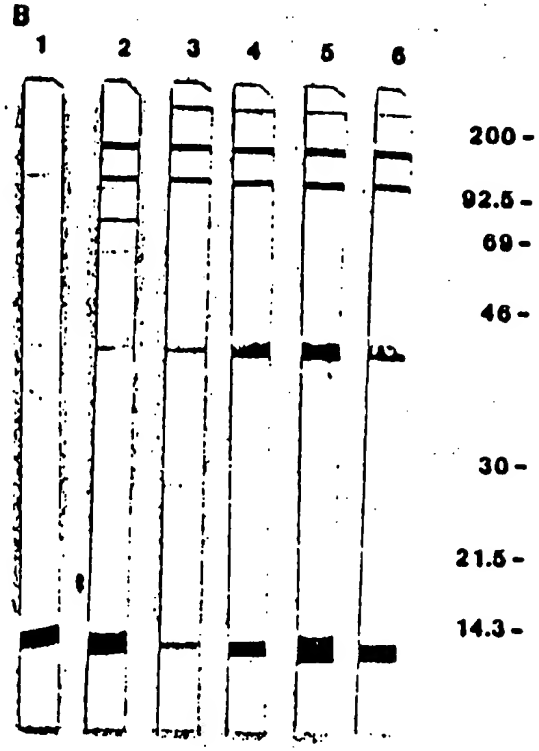


Fig. 3C

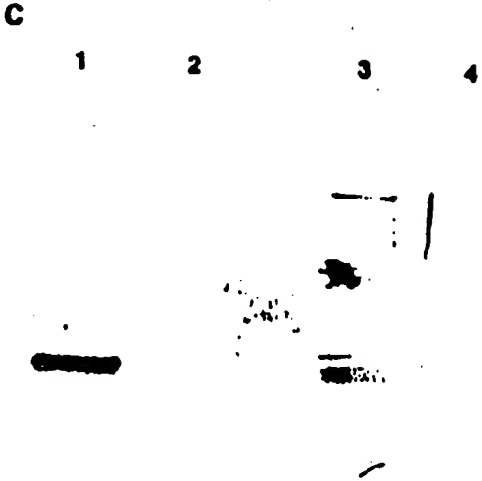


Fig. 4

Fig. 4A

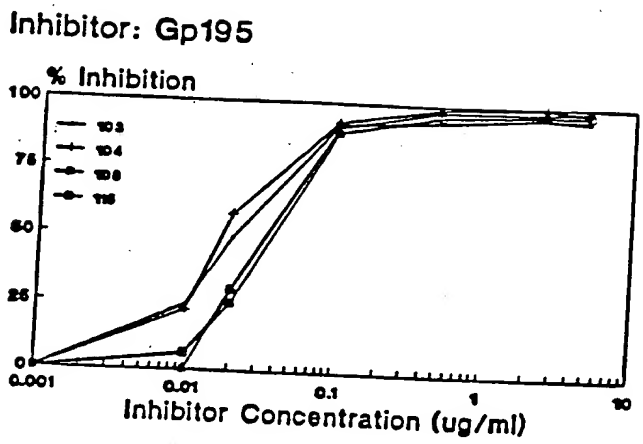


Fig. 4B

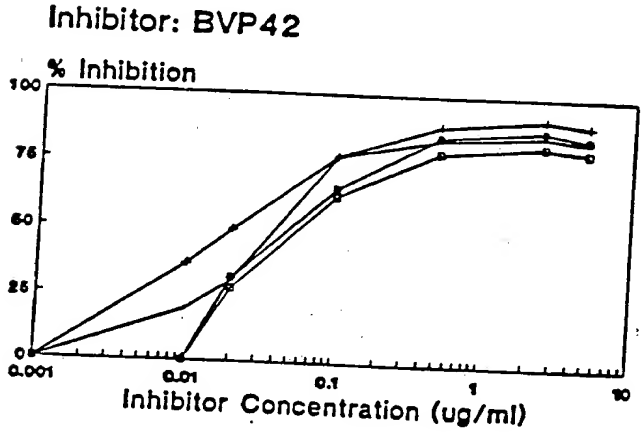


Fig. 4C

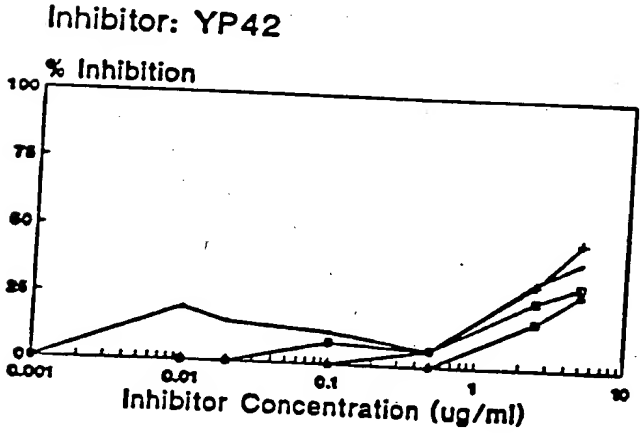
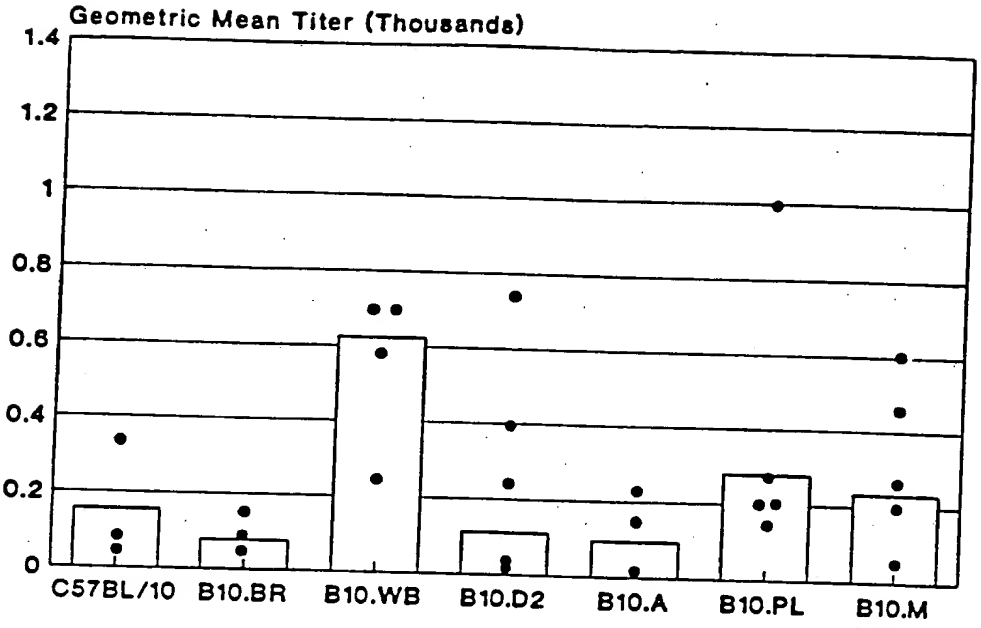


Fig. 5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1
0.8
0.6
0.4
0.2
0
C57BL/10
B10.BR
B10.WB
B10.D2
B10.A
B10.PL
B10.M

Fig. 6

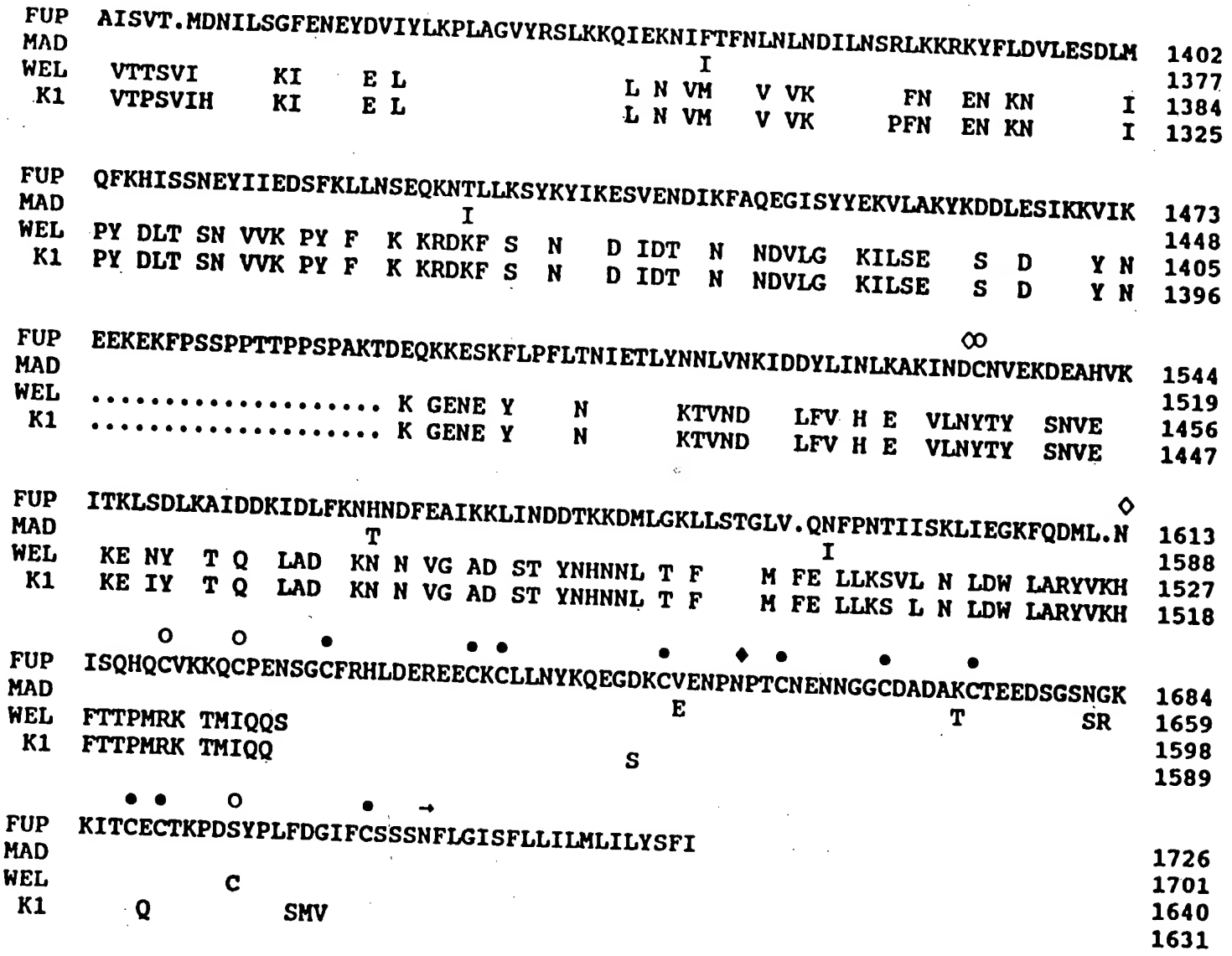
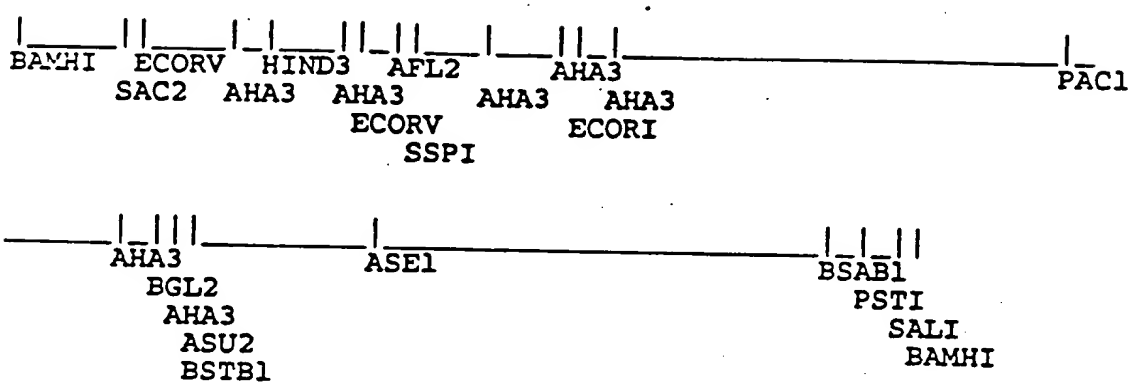


Fig. 7A

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                  MetTrpSerTrpLysCysLeuLeuPheTrpAlaValLeuValThrAla
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    CCTAGGTGACCCTACACCTCGACCTTCACGGAGGAGAAGACCCGACAGGACCAGTGTCGG

    1 BAMHI,

                  V
    ThrLeuCysThrAlaAlaIleSerValThrMetAspAsnIleLeuSerGlyPheGluAsn
 61 ACACTCTGCACCGCGGCGATATCTGTCACAATGGATAATATCCTCTCAGGATTTGAAAAT
    TGTGAGACGTGGCGCCGCTATAGACAGTGTTACCTATTATAGGAGAGTCCTAAACTTTTA

    71 SAC2, 78 ECORV,

    GluTyrAspValIleTyrLeuLysProLeuAlaGlyValTyrArgSerLeuLysLysGln
121 GAATATGATGTTATATATTTAAAACCTTTAGCTGGAGTATATAGAAGCTTAAAAAAACAA
    CTTATACTACAATATATAAATTTTGGAAATCGACCTCATATATCTTCGAATTTTTTTGTT

    138 AHA3, 165 HIND3,

    IleGluLysAsnIlePheThrPheAsnLeuAsnLeuAsnAspIleLeuAsnSerArgLeu
181 ATTGAAAAAAACATTTTTACATTTAATTTAAATTTGAACGATATCTTAAATTCACGTCTT
    TAACTTTTTTTGTAAAAATGTAAATTAAATTTAAACTTGCTATAGAATTTAAGTGCAGAA

    207 AHA3, 220 ECORV, 238 AFL2,

    LysLysArgLysTyrPheLeuAspValLeuGluSerAspLeuMetGlnPheLysHisIle
241 AAGAAACGAAAATATTTCTTAGATGTATTAGAATCTGATTTAATGCAATTTAAACATATA
    TTCTTTGCTTTTATAAAGAATCTACATAATCTTAGACTAAATTACGTTAAATTTGTATAT

    251 SSPI, 289 AHA3,

    SerSerAsnGluTyrIleIleGluAspSerPheLysLeuLeuAsnSerGluGlnLysAsn
```

Fig. 7B

```
301  TCCTCAAATGAATACATTATTGAAGATTCATTTAAATTATTGAATTCAGAACAAAAAAAC
     AGGAGTTTACTTATGTAATAACTTCTAAGTAAATTTAATAACTTAAGTCTTGTTTTTTTG

     331 AHA3, 342 ECORI,

     ThrLeuLeuLysSerTyrLysTyrIleLysGluSerValGluAsnAspIleLysPheAla
361  ACACTTTTAAAAAGTTACAAATATATAAAAGAATCAGTAGAAAATGATATTAAATTTGCA
     TGTGAAAATTTTTCAATGTTTATATATTTTCTTAGTCATCTTTTACTATAATTTAAACGT

     366 AHA3,

     GlnGluGlyIleSerTyrTyrGluLysValLeuAlaLysTyrLysAspAspLeuGluSer
421  CAGGAAGGTATAAGTTATTATGAAAAGGTTTTAGCGAAATATAAGGATGATTTAGAATCA
     GTCCTTCCATATTCAATAATACTTTTCCAAAATCGCTTTATATTCCTACTAAATCTTAGT

     IleLysLysValIleLysGluGluLysGluLysPheProSerSerProProThrThrPro
481  ATTAAAAAAGTTATCAAAGAAGAAAAGGAGAAGTTCCCATCATCACCACCAACAACACCT
     TAATTTTTTCAATAGTTTCTTCTTTTCCTCTTCAAGGGTAGTAGTGGTGGTTGTTGTGGA

     ProSerProAlaLysThrAspGluGlnLysLysGluSerLysPheLeuProPheLeuThr
541  CCGTCACCAGCAAAAACAGACGAACAAAAGAAGGAAAGTAAGTTCCTTCCATTTTTAACA
     GGCAGTGGTCGTTTTTGTCTGCTTGTTTTCTTCCTTTCATTCAAGGAAGGTAAAAATTGT

     AsnIleGluThrLeuTyrAsnAsnLeuValAsnLysIleAspAspTyrLeuIleAsnLeu
601  AACATTGAGACCTTATACAATAACTTAGTTAATAAAATTGACGATTACTTAATTAACTTA
     TTGTAACTCTGGAATATGTTATTGAATCAATTATTTTAACTGCTAATGAATTAATTGAAT

     649 PACl,

     LysAlaLysIleAsnAspCysAsnValGluLysAspGluAlaHisValLysIleThrLys
661  AAGGCAAAGATTAACGATTGTAATGTTGAAAAAGATGAAGCACATGTTAAAATAACTAAA
     TTCCGTTTCTAATTGCTAACATTACAACTTTTTCTACTTCGTGTACAATTTTATTGATTT

     LeuSerAspLeuLysAlaIleAspAspLysIleAspLeuPheLysAsnHisAsnAspPhe
721  CTTAGTGATTTAAAAGCAATTGATGACAAAATAGATCTTTTTAAAAACCATAACGACTTC
     GAATCACTAAATTTTCGTTAACTACTGTTTTATCTAGAAAAATTTTTGGTATTGCTGAAG

     729 AHA3, 753 BGL2, 760 AHA3, 778 ASU2 BSTBl,

     GluAlaIleLysLysLeuIleAsnAspAspThrLysLysAspMetLeuGlyLysLeuLeu
781  GAAGCAATTAAAAAATTGATAAATGATGATACGAAAAAAGATATGCTTGGCAAATTACTT
     CTTCGTTAATTTTTTAACTATTTACTACTATGCTTTTTTCTATACGAACCGTTTAATGAA

     SerThrGlyLeuValGlnAsnPheProAsnThrIleIleSerLysLeuIleGluGlyLys
841  AGTACAGGATTAGTTCAAAATTTTCCTAATACAATAATATCAAAATTAATTGAAGGAAAA
     TCATGTCCTAATCAAGTTTTAAAAGGATTATGTTATTATAGTTTTAATTAACTTCCTTTT

     885 ASEl,

     PheGlnAspMetLeuAsnIleSerGlnHisGlnCysValLysLysGlnCysProGluAsn
901  TTCCAAGATATGTTAAACATTTCACAACACCAATGCGTAAAAAAACAATGTCCAGAAAAT
     AAGGTTCTATACAATTTGTAAAGTGTTGTGGTTACGCATTTTTTTGTTACAGGTCTTTTA

     SerGlyCysPheArgHisLeuAspGluArgGluGluCysLysCysLeuLeuAsnTyrLys
961  TCTGGATGTTTCAGACATTTAGATGAAAGAGAAGAATGTAAATGTTTATTAAATTACAAA
     AGACCTACAAAGTCTGTAAATCTACTTTCTCTTCTTACATTTACAAATAATTTAATGTTT
```

Fig. 7C

```
       GlnGluGlyAspLysCysValGluAsnProAsnProThrCysAsnGluAsnAsnGlyGly
1021   CAAGAAGGTGATAAATGTGTTGAAAATCCAAATCCTACTTGTAACGAAAATAATGGTGGA
       GTTCTTCCACTATTTACACAACTTTTAGGTTTAGGATGAACATTGCTTTTATTACCACCT

       CysAspAlaAspAlaLysCysThrGluGluAspSerGlySerAsnGlyLysLysIleThr
1081   TGTGATGCAGATGCCAAATGTACCGAAGAAGATTCAGGTAGCAACGGAAAGAAAATCACA
       ACACTACGTCTACGGTTTACATGGCTTCTTCTAAGTCCATCGTTGCCTTTCTTTTAGTGT

       CysGluCysThrLysProAspSerTyrProLeuPheAspGlyIlePheCysSerAM AM
1141   TGTGAATGTACTAAACCTGATTCTTATCCACTTTTCGATGGTATTTTCTGCAGTTAGTAG
       ACACTTACATGATTTGGACTAAGAATAGGTGAAAAGCTACCATAAAAGACGTCAATCATC

       1159 BSAB1, 1188 PSTI, 1200 SALI,

1201   TCGACCCTTGGAAGGATCC
       AGCTGGGAACCTTCCTAGG

       1214 BAMHI,

1261
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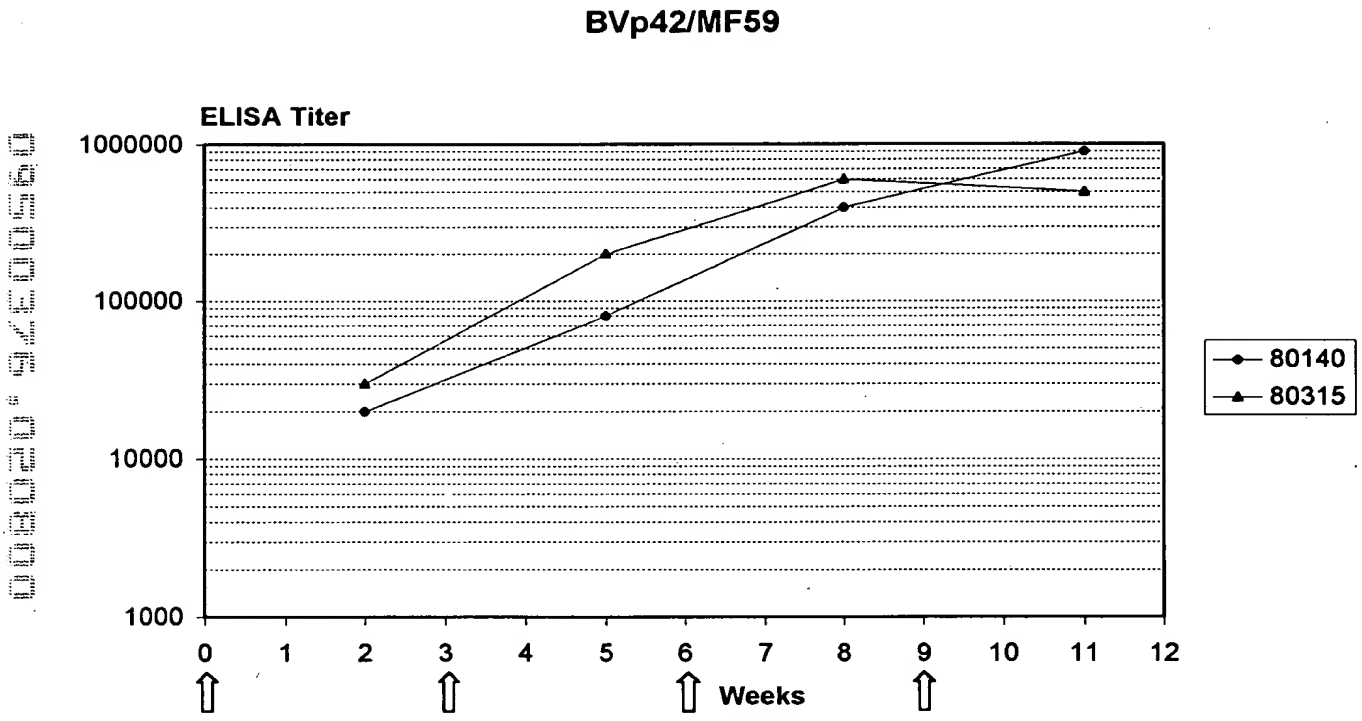
09503763 . 020800

Figure 8A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100000
10000
1000
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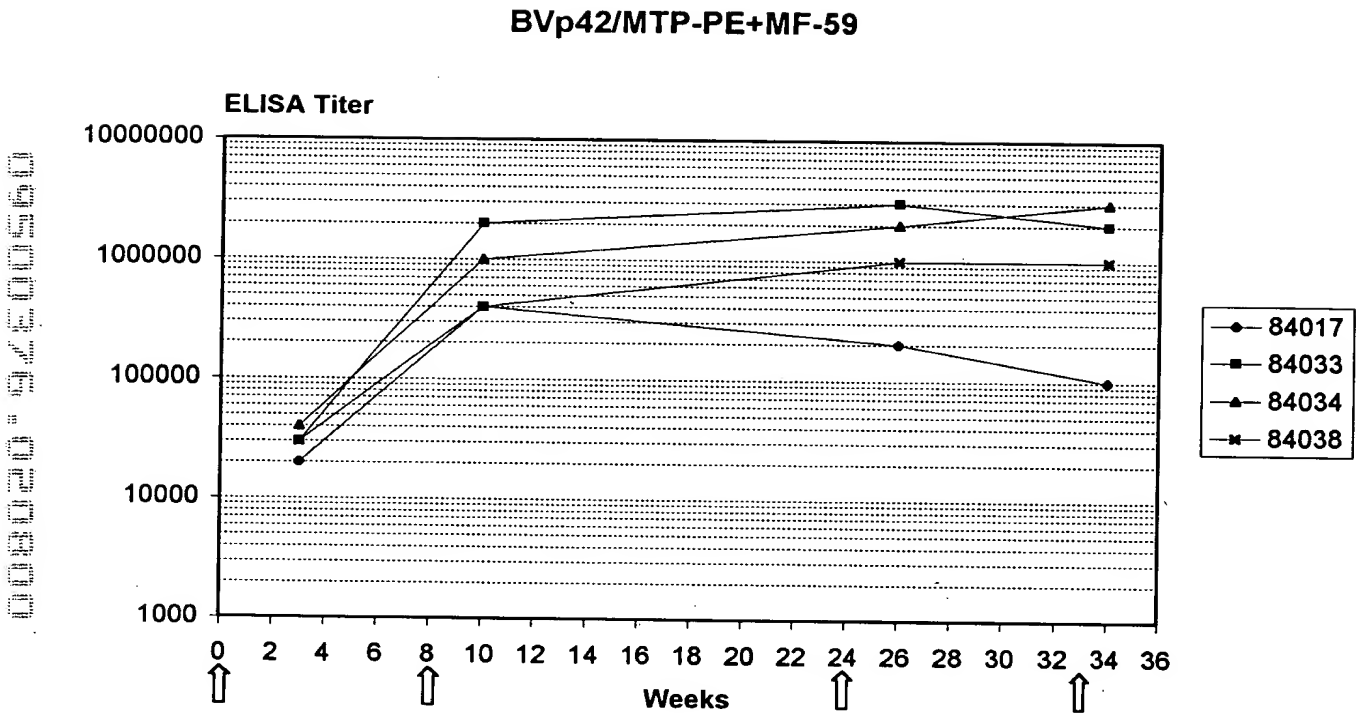
Weeks
80140
80315

Figure 8B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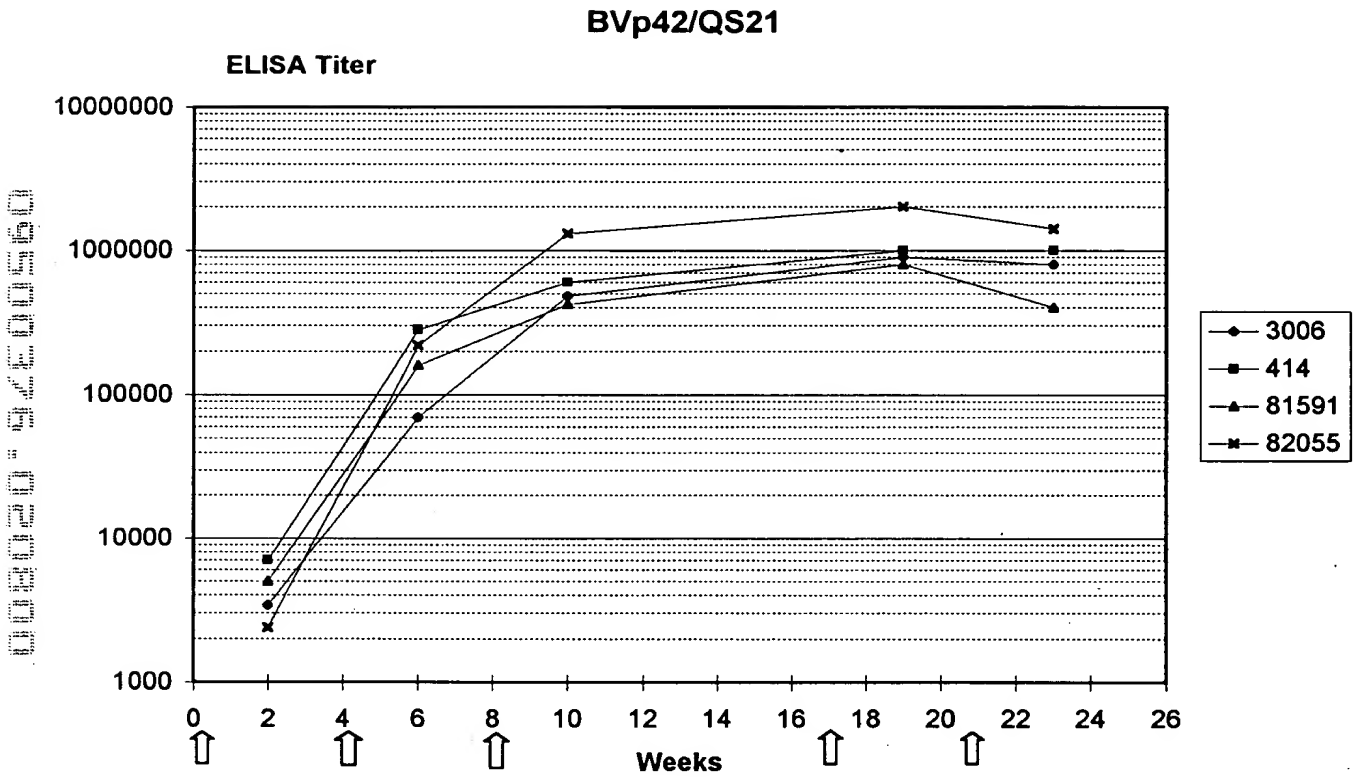
ELISA Titer
10000000
1000000
100000
10000
1000
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36
Weeks
84017
84033
84034
84038

Figure 8C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ELISA Titer
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Weeks
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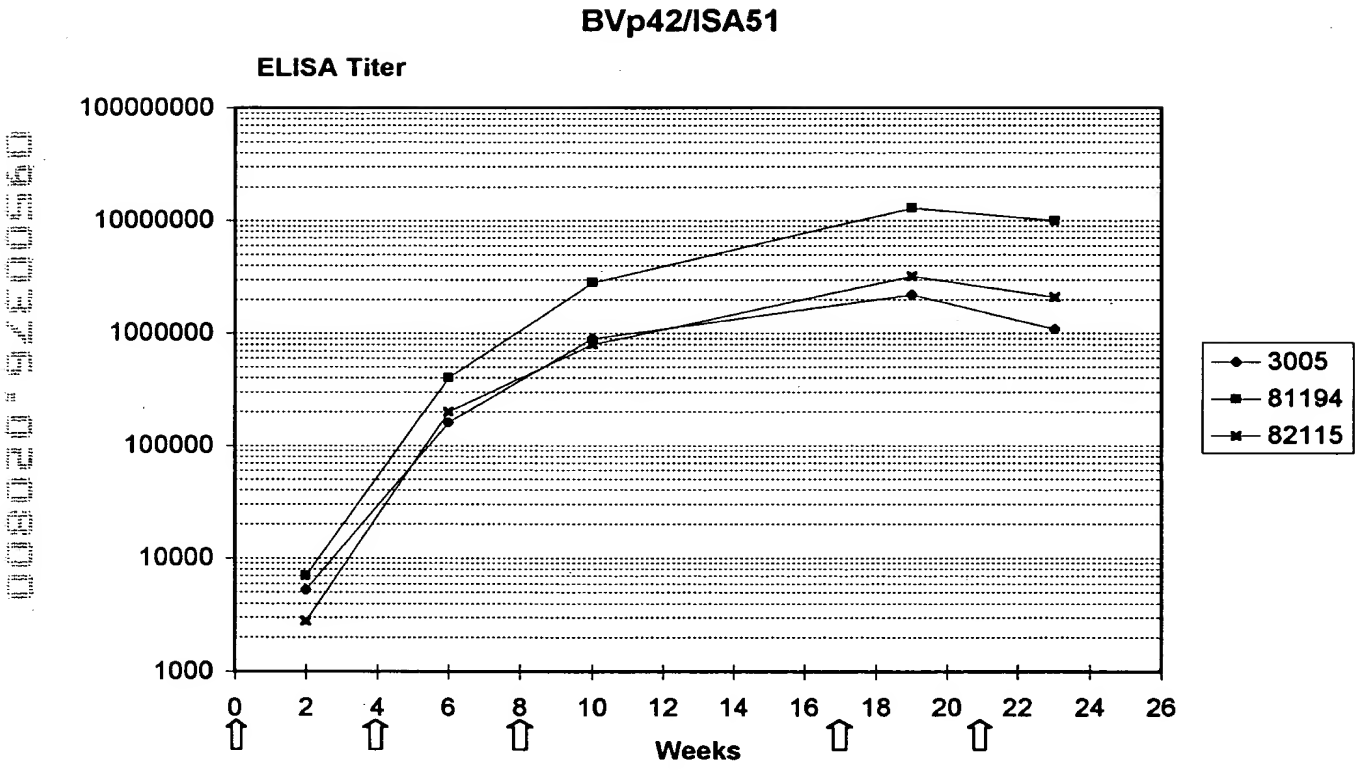
81591
82055

Figure 8D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ELISA Titer
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12
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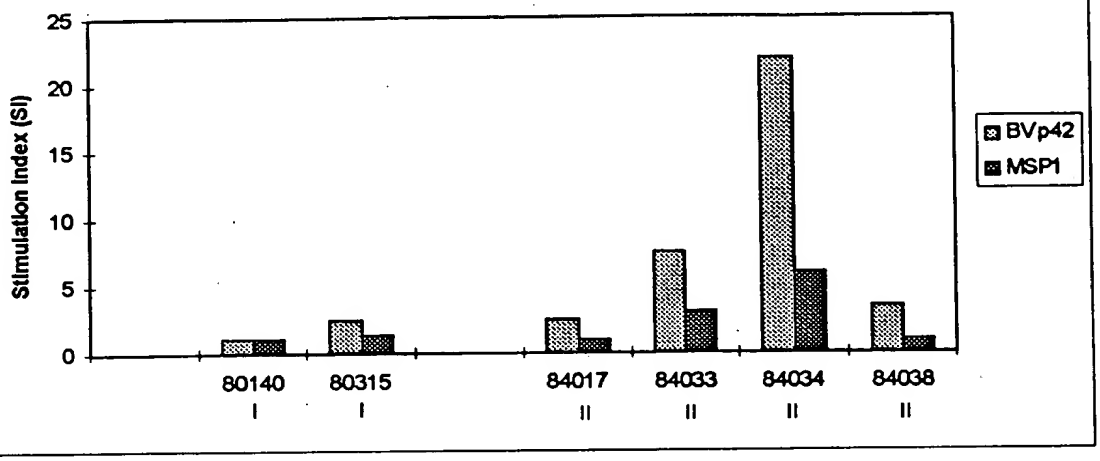
16
18
20
22
24
26
Weeks
3005
81194
82115

FIGURE 9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5
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BVp42
MSP1
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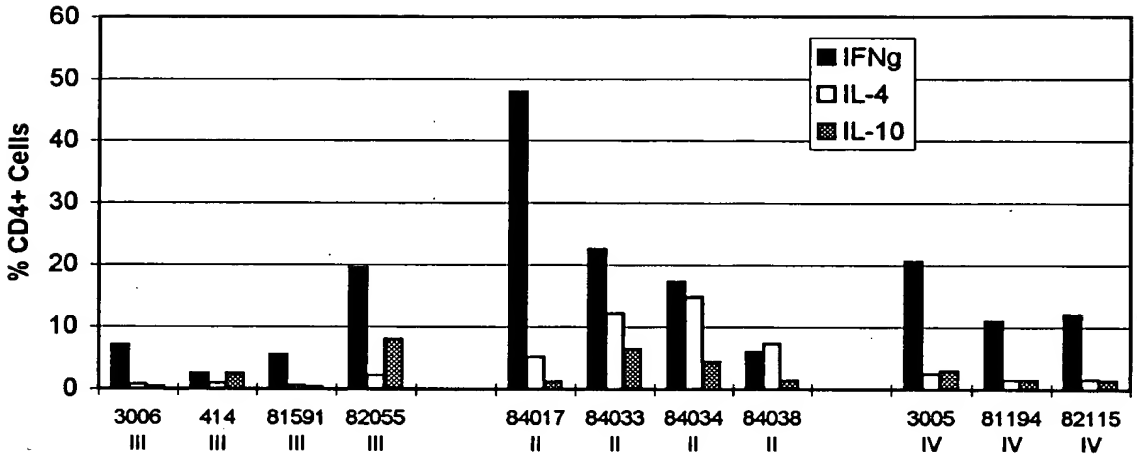
I
80315
I
84017
II
84033
II
84034
II
84038
II

FIGURE 10A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40
30
20
10
0
% CD4+ Cells
IFNg
IL-4
IL-10
3006 III
414 III
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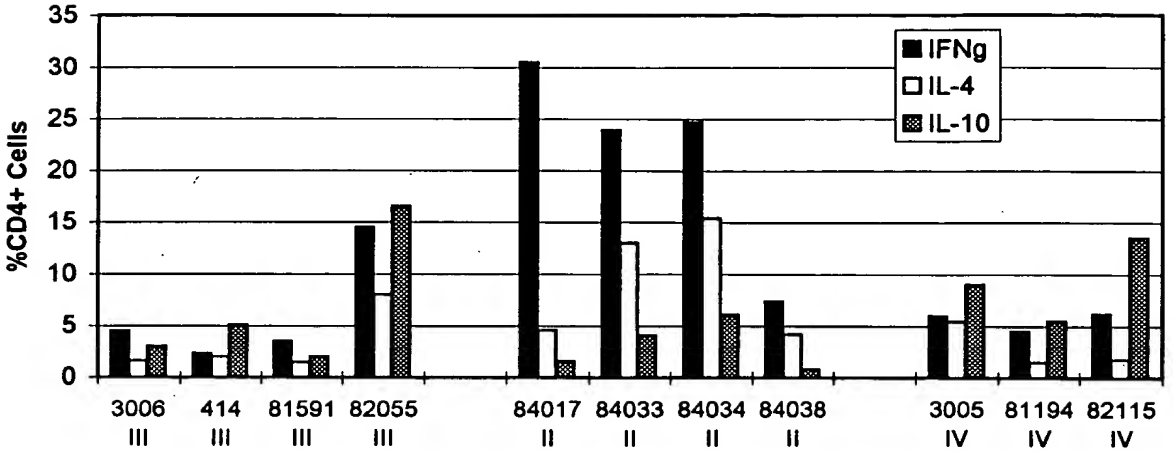
82055 III
84017 II
84033 II
84034 II
84038 II
3005 IV
81194 IV
82115 IV

FIGURE 10B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30
25
20
15
10
5
0
%CD4+ Cells
IFNg
IL-4
IL-10
3006 III
414 III
81591 III
82055 III
84017 II
84033 II
84034 II
84038 II
3005 IV
81194 IV
82115 IV

FIGURE 11A

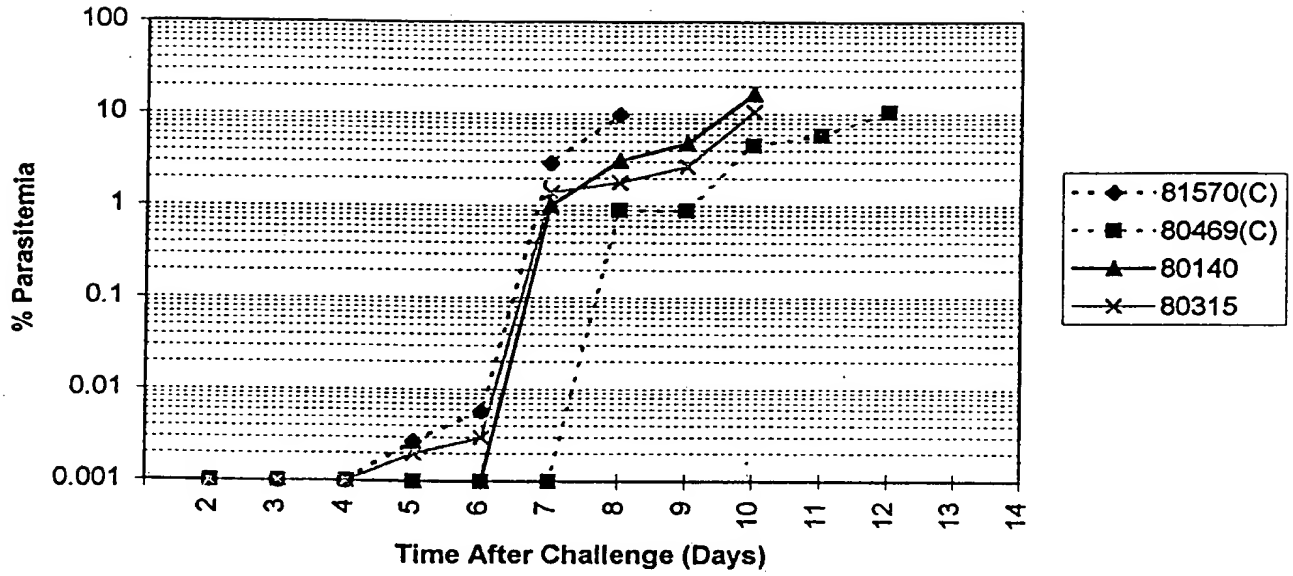

FIGURE 11B

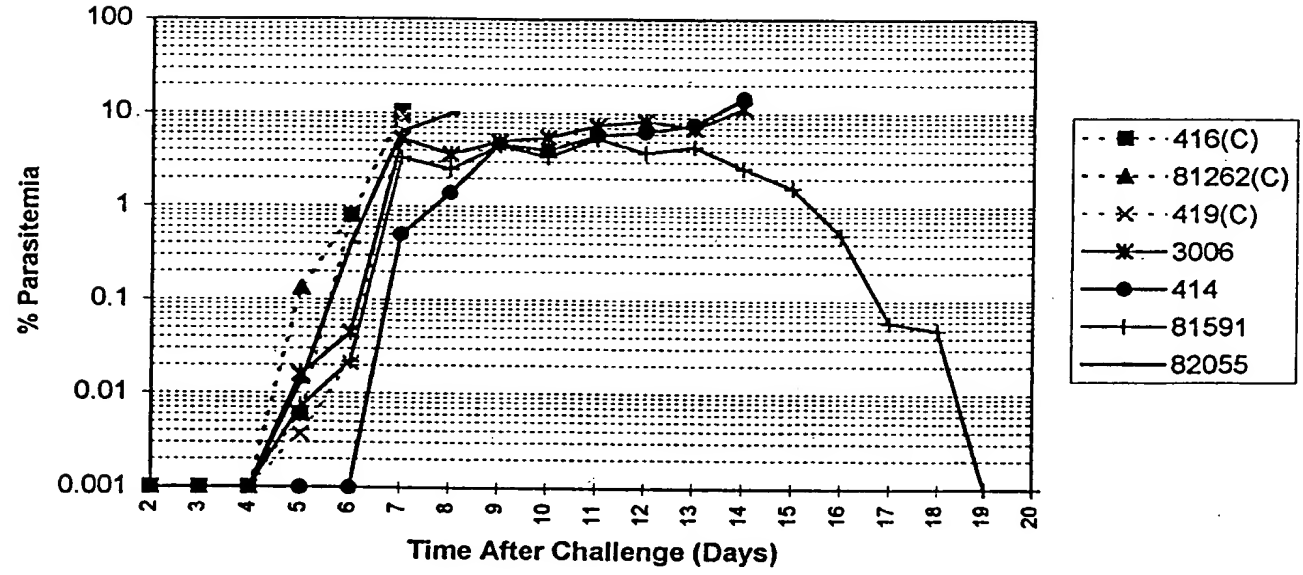

FIGURE 11C

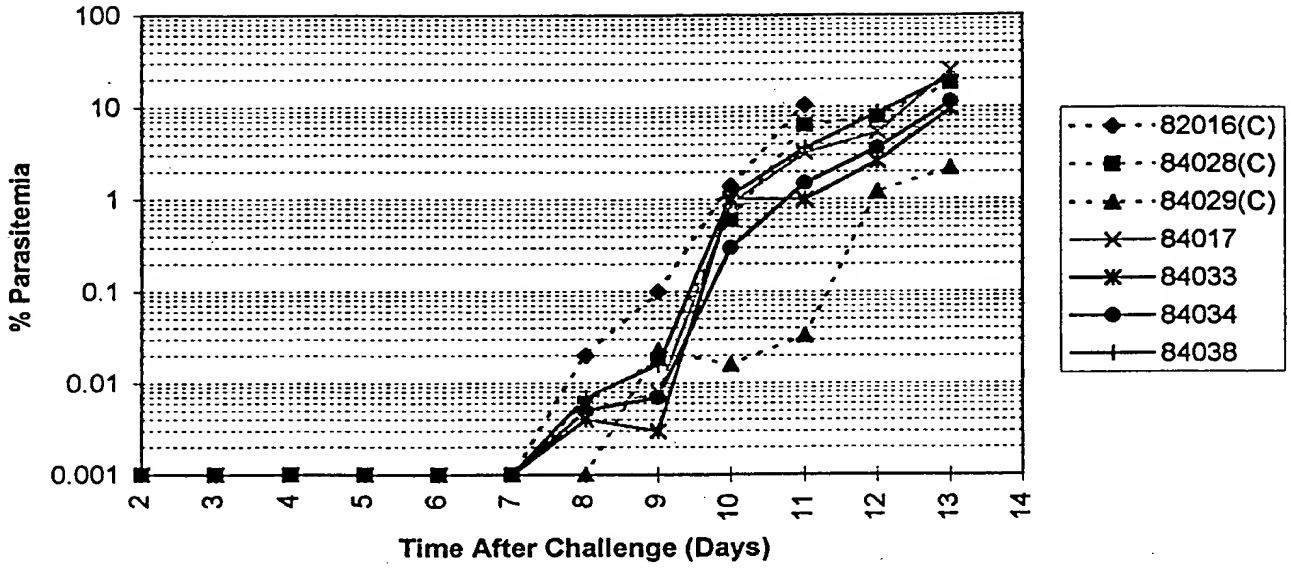

FIGURE 11D

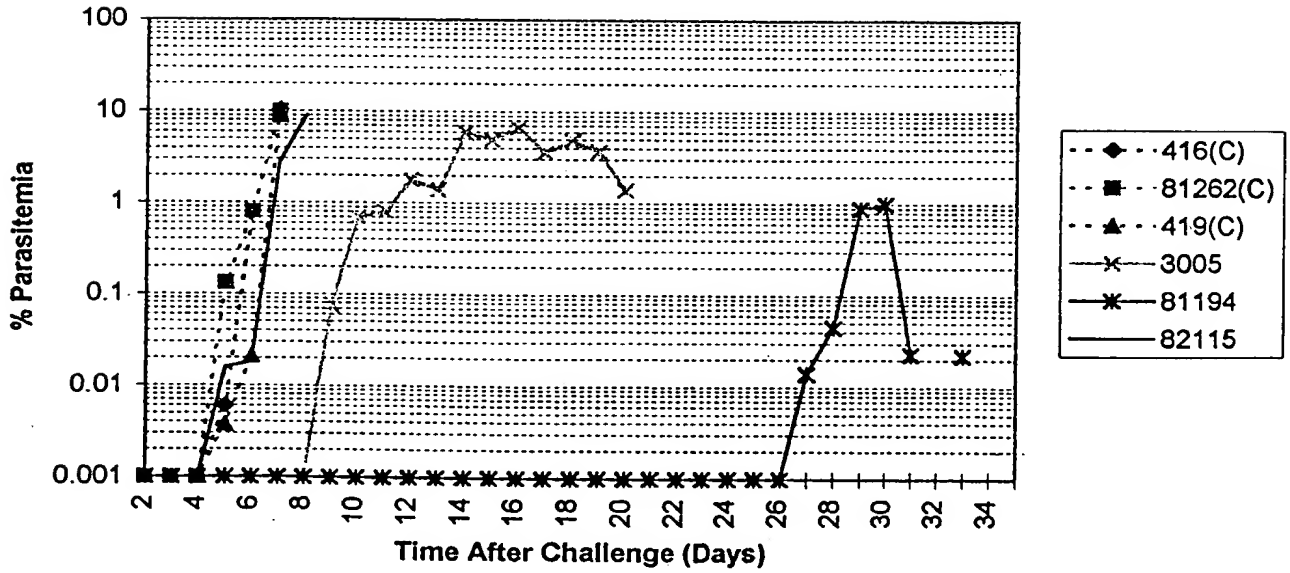

FIGURE 12

DNA AND AMINO ACID SEQUENCE OF BVp42-M

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  58 gccactctttgcacagcagcgatctctgttactatggacaacatc
     A  T  L  C  T  A  A  I  S  V  T  M  D  N  I
 103 ctcagtggcttcgagaacgagtacgacgtaatctacctaaagccc
     L  S  G  F  E  N  E  Y  D  V  I  Y  L  K  P
 148 cttgccggtgtctaccgttcattgaagaaacagatagaaaagaat
     L  A  G  V  Y  R  S  L  K  K  Q  I  E  K  N
 193 attttcacgttcaacctcaacctaaatgacatcctcaactcgcgc
     I  F  T  F  N  L  N  L  N  D  I  L  N  S  R
 238 ctcaagaagcgaaaatacttcctcgacgtgttggaatccgacctt
     L  K  K  R  K  Y  F  L  D  V  L  E  S  D  L
 283 atgcaatttaagcacattagctctaacgagtacatcatagaggac
     M  Q  F  K  H  I  S  S  N  E  Y  I  I  E  D
 328 agcttcaagctcttgaattcagaacagaagaacaccctcctaaag
     S  F  K  L  L  N  S  E  Q  K  N  T  L  L  K
 373 tcctacaaatacattaaggagtctgttgagaacgacatcaagttc
     S  Y  K  Y  I  K  E  S  V  E  N  D  I  K  F
 418 gcccaggaaggaattagctactatgagaaagtcctggctaaatac
     A  Q  E  G  I  S  Y  Y  E  K  V  L  A  K  Y
 463 aaggacgacttggaaagcattaagaaggtaatcaaagaagagaag
     K  D  D  L  E  S  I  K  K  V  I  K  E  E  K
 508 gaaaagtttccgagctctccacccacaactcccccatcgcctgca
     E  K  F  P  S  S  P  P  T  T  P  P  S  P  A
 553 aagaccgacgagcagaaaaaagaaagtaagttccttccattcctc
     K  T  D  E  Q  K  K  E  S  K  F  L  P  F  L
 598 accaacatcgaaactctatataacaacctggtgaacaagattgat
     T  N  I  E  T  L  Y  N  N  L  V  N  K  I  D
 643 gactacttaatcaacttgaaggcgaaaattaatgactgtaacgtc
     D  Y  L  I  N  L  K  A  K  I  N  D  C  N  V
 688 gaaaaggatgaagcccacgttaagatcaccaagctttccgatctc
     E  K  D  E  A  H  V  K  I  T  K  L  S  D  L
 733 aaagccatcgacgataagattgacctgtttaagaaccacaacgat
     K  A  I  D  D  K  I  D  L  F  K  N  H  N  D
 778 ttcgacgcaatcaaaaagttgatcaacgacgatactaagaaagac
     F  D  A  I  K  K  L  I  N  D  D  T  K  K  D
 823 atgcttggaaaactgctgtcgacaggcttggtccaaaacttcccg
     M  L  G  K  L  L  S  T  G  L  V  Q  N  F  P
 868 aacaccattataagcaagctgatcgaaggaaagtttcaggatatg
```

FIGURE 12

```
          N   T   I   I   S   K   L   I   E   G   K   F   Q   D   M
      913 ctgaacatctctcagcatcaatgcgtgaagaagcaatgtcccgag
          L   N   I   S   Q   H   Q   C   V   K   K   Q   C   P   E
      958 aattcaggttgcttccgccacttagacgaaagggaggaatgtaaa
          N   S   G   C   F   R   H   L   D   E   R   E   E   C   K
     1003 tgcctgctgaattataaacaggaaggagacaagtgcgtagagaat
          C   L   L   N   Y   K   Q   E   G   D   K   C   V   E   N
     1048 cctaacccaacctgtaacgaaaataacggtggctgcgatgctgac
          P   N   P   T   C   N   E   N   N   G   G   C   D   A   D
     1093 gctaagtgtaccgaggaggacagcggttccaatggcaagaaaata
          A   K   C   T   E   E   D   S   G   S   N   G   K   K   I
     1138 acttgcgaatgcacgaagcccgatagttaccctctcttcgacggt
          T   C   E   C   T   K   P   D   S   Y   P   L   F   D   G
     1183 atcttctgctcc
          I   F   C   S

ccacctcatcatcatcatcatcattaataaggtaccta
P   P   H   H   H   H   H   H   *   *
```

FIGURE 14

DNA AND AMINO ACID SEQUENCE OF P42-K

```
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                 M  W  S  W  K  C  L  L  F  W  A  V  L
  51 GTCACAGCCACACTCTGCACCGCGGGCGCCGCAGTAACTCCTTCCGTAAT
     V  T  A  T  L  C  T  A  G  A  A  V  T  P  S  V  I
 101 TGATAACATACTTTCTAAAATTGAAAATGAATATGAGGTTTTATATTTAA
      D  N  I  L  S  K  I  E  N  E  Y  E  V  L  Y  L
 151 AACCTTTAGCAGGTGTTTATAGAAGTTTAAAAAAACAATTAGAAAATAAC
     K  P  L  A  G  V  Y  R  S  L  K  K  Q  L  E  N  N
 201 GTTATGACATTTAATGTTAATGTTAAGGATATTTTAAATTCACGATTTAA
      V  M  T  F  N  V  N  V  K  D  I  L  N  S  R  F  N
 251 TAAACGTGAAAATTTCAAAAATGTTTTAGAATCAGATTTAATTCCATATA
       K  R  E  N  F  K  N  V  L  E  S  D  L  I  P  Y
 301 AAGATTTAACATCAAGTAATTATGTTGTCAAAGATCCATATAAATTTCTT
     K  D  L  T  S  S  N  Y  V  V  K  D  P  Y  K  F  L
 351 AATAAAGAAAAAAGAGATAAATTCTTAAGCAGTTATAATTATATTAAGGA
      N  K  E  K  R  D  K  F  L  S  S  Y  N  Y  I  K  D
 401 TTCAATAGATACGGATATAAATTTTGCAAATGATGTTCTTGGATATTATA
       S  I  D  T  D  I  N  F  A  N  D  V  L  G  Y  Y
 451 AAATATTATCCGAAAAATATAAATCAGATTTAGATTCAATTAAAAAATAT
     K  I  L  S  E  K  Y  K  S  D  L  D  S  I  K  K  Y
 501 ATCAACGACAAACAAGGTGAAAATGAGAAATACCTTCCCTTTTTAAACAA
      I  N  D  K  Q  G  E  N  E  K  Y  L  P  F  L  N  N
 551 TATTGAGACCTTATATAAAACAGTTAATGATAAAATTGATTTATTTGTAA
       I  E  T  L  Y  K  T  V  N  D  K  I  D  L  F  V
 601 TTCATTTAGAAGCAAAAGTTCTAAATTATACATATGAGAAATCAAACGTA
     I  H  L  E  A  K  V  L  N  Y  T  Y  E  K  S  N  V
 651 GAAGTTAAAATAAAAGAACTTAATTACTTAAAAACAATTCAAGACAAATT
      E  V  K  I  K  E  L  N  Y  L  K  T  I  Q  D  K  L
 701 GGCAGATTTTAAAAAAAATAACAATTTCGTTGGAATTGCTGATTTATCAA
       A  D  F  K  K  N  N  N  F  V  G  I  A  D  L  S
 751 CAGATTATAACCATAATAACTTATTGACAAAGTTCCTTAGTACAGGTATG
     T  D  Y  N  H  N  N  L  L  T  K  F  L  S  T  G  M
```

```
801 GTTTTTGAAAATCTTGCTAAAACCGTTTTATCTAATTTACTTGATGGAAA
     V  F  E  N  L  A  K  T  V  L  S  N  L  L  D  G  N
851 CTTGCAAGGTATGTTAAACATTTCACAACACCAATGCGTAAAAAAACAAT
      L  Q  G  M  L  N  I  S  Q  H  Q  C  V  K  K  Q
901 GTCCACAAAATTCTGGATGTTTCAGACATTTAGATGAAAGAGAAGAATGT
    C  P  Q  N  S  G  C  F  R  H  L  D  E  R  E  E  C
951 AAATGTTTATTAAATTACAAACAAGAAGGTGATAAATGTGTTGAAAATCC
     K  C  L  L  N  Y  K  Q  E  G  D  K  C  V  E  N  P
1001 AAATCCTACTTGTAACGAAAATAATGGTGGATGTGATGCAGATGCCAAAT
      N  P  T  C  N  E  N  N  G  G  C  D  A  D  A  K
1051 GTACCGAAGAAGATTCAGGTAGCAACGGAAAGAAAATCACATGTGAATGT
    C  T  E  E  D  S  G  S  N  G  K  K  I  T  C  E  C
1101 ACTAAACCTGATTCTTATCCACTTTTCGATGGTATTTTCTGCAGTCATCA
     T  K  P  D  S  Y  P  L  F  D  G  I  F  C  S  H  H
1151 TCATCATCATCATTAATAAGGTACC
      H  H  H  H  *  *
```

Underlined sequences represent restriction sites.
Bold letters represent alterations done to the leader sequence as described in the methods.
The boxed letter represents the original sequence where a mis-sense mutation to a cytosine occurred.
"*" represent stop codons.

FIGURE 14

FIGURE 15

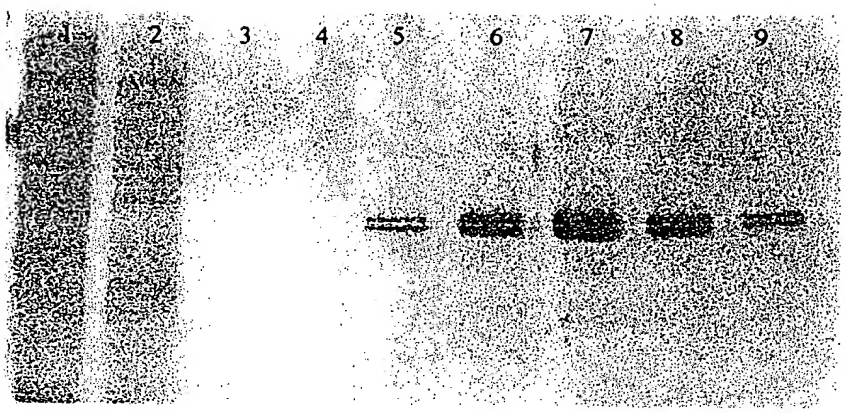

FIGURE 16

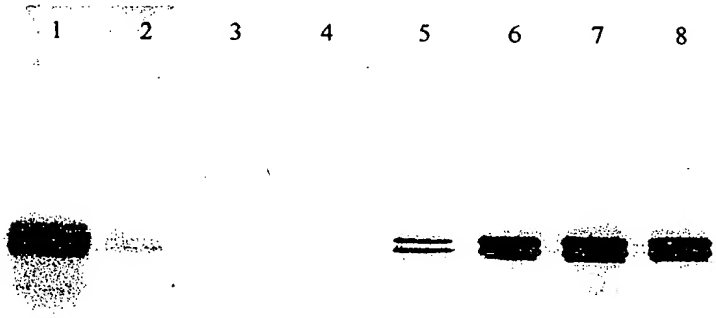

FIGURE 17

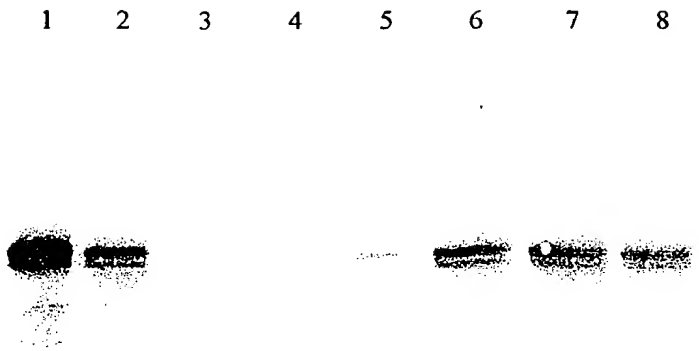

FIGURE 20

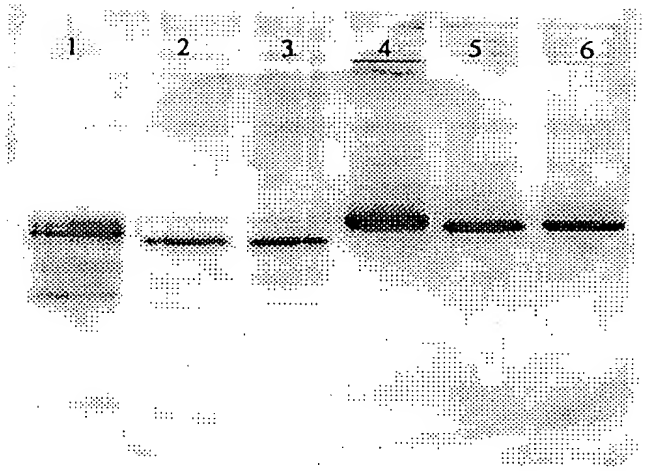

FIGURE 18A

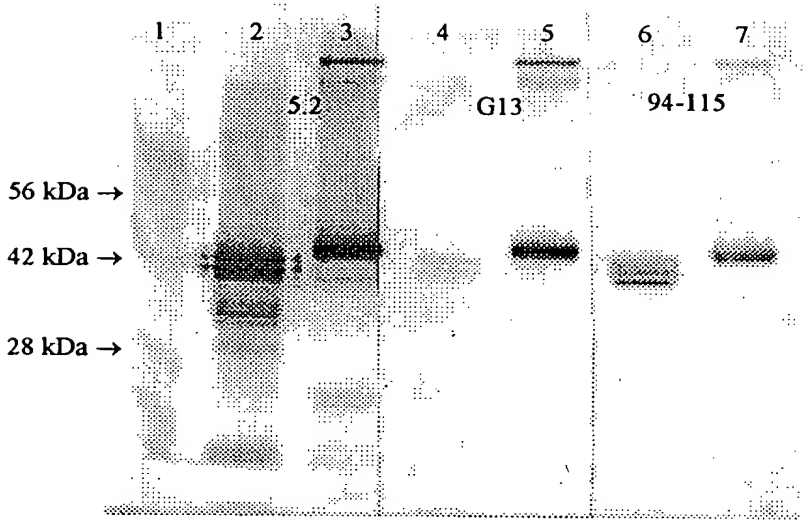

FIGURE 18B

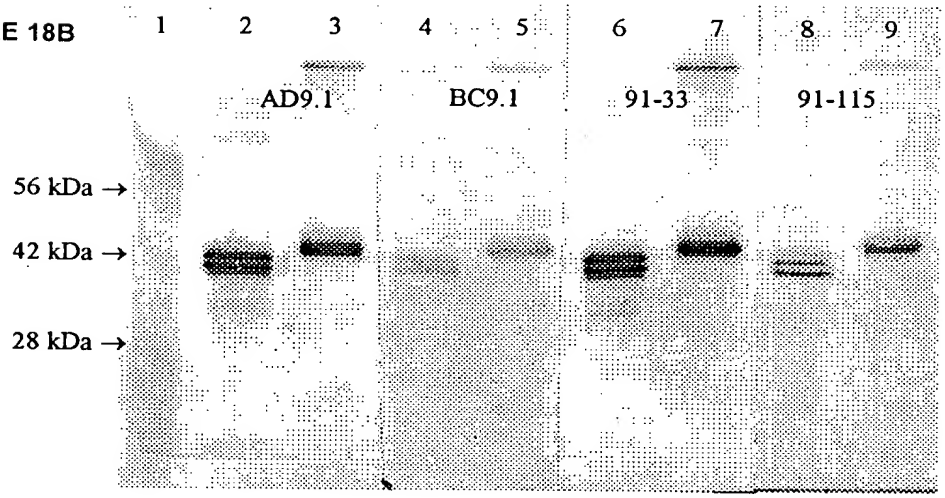

FIGURE 19A

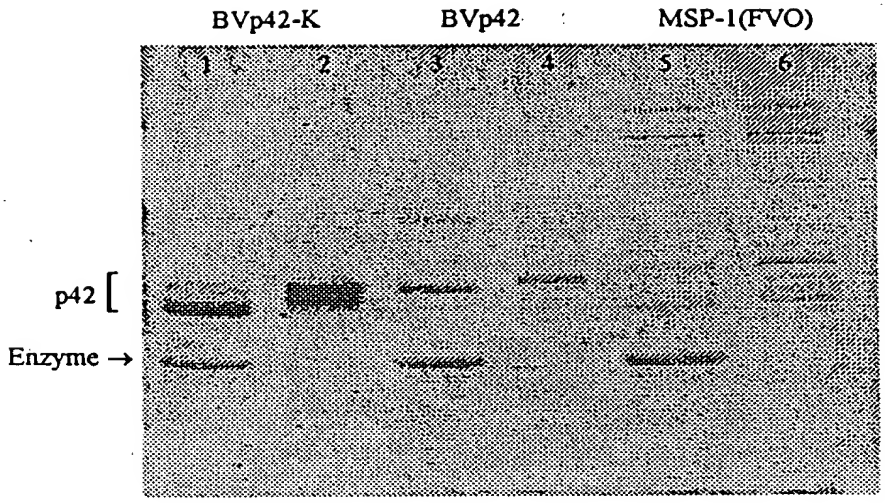

FIGURE 19B